

# Package ‘LOBSTAHS’

June 27, 2022

**Title** Lipid and Oxylipin Biomarker Screening through Adduct Hierarchy Sequences

**Version** 1.23.0

**Date** 2021-08-30

**Depends** R (>= 3.4), xcms, CAMERA, methods

**Imports** utils

**Suggests** PtH2O2lipids, knitr, rmarkdown

**Description** LOBSTAHS is a multifunction package for screening, annotation, and putative identification of mass spectral features in large, HPLC-MS lipid datasets. In silico data for a wide range of lipids, oxidized lipids, and oxylipins can be generated from user-supplied structural criteria with a database generation function. LOBSTAHS then applies these databases to assign putative compound identities to features in any high-mass accuracy dataset that has been processed using xcms and CAMERA. Users can then apply a series of orthogonal screening criteria based on adduct ion formation patterns, chromatographic retention time, and other properties, to evaluate and assign confidence scores to this list of preliminary assignments. During the screening routine, LOBSTAHS rejects assignments that do not meet the specified criteria, identifies potential isomers and isobars, and assigns a variety of annotation codes to assist the user in evaluating the accuracy of each assignment.

**License** GPL (>= 3) + file LICENSE

**URL** <http://bioconductor.org/packages/LOBSTAHS>

**BugReports** <https://github.com/vanmooylipidomics/LOBSTAHS/issues/new>

**VignetteBuilder** knitr

**biocViews** ImmunoOncology, MassSpectrometry, Metabolomics, Lipidomics, DataImport

**NeedsCompilation** no

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**git\_url** <https://git.bioconductor.org/packages/LOBSTAHS>

**git\_branch** master

**git\_last\_commit** d67c139

**git\_last\_commit\_date** 2022-04-26

**Date/Publication** 2022-06-27

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doLOBscreen	<i>Screen, annotate, and identify compounds in an xsAnnotate object</i>
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## Description

Primary function of the LOBSTAHS package. Screen, annotate, and assign compound identities to peak groups in a CAMERA [xsAnnotate](#) object containing HPLC-ESI-MS lipid data. Identify and annotate possible isomers and isobars.

## Usage

```
doLOBscreen(xsA, polarity = NULL, database = NULL, remove.iso = TRUE,
            rt.restrict = TRUE, rt.windows = NULL, exclude.oddFA = TRUE,
            exclude.oxyrule = TRUE, match.ppm = NULL, retain.unidentified = TRUE)
```

**Arguments**

<code>xsA</code>	A CAMERA <code>xsAnnotate-class</code> object with identified pseudospectra. Must contain isotope data from <code>findIsotopes</code> if user elects <code>remove.iso = TRUE</code> .
<code>polarity</code>	Specify polarity mode of data in <code>xsA</code> : "positive" or "negative." doLOBscreen will attempt to detect the polarity mode if nothing is given.
<code>database</code>	Specify the LOBdbase from which compound identities and adduct ion hierarchy data are to be applied. If nothing is specified, doLOBscreen will use the LOBSTAHS default database ( <code>default.LOBdbase</code> ) for the appropriate ionization mode.  The database generation function <code>generateLOBdbase</code> can be used to create a LOBdbase from structural property ranges specified by the user in a series of input tables. <code>loadLOBdbase</code> can be used to import and reconstruct a "LOBdbase" object from a previously generated database that was saved as a .csv file.
<code>remove.iso</code>	Should secondary isotope peaks be removed? (If TRUE, <code>xsA</code> must contain isotope data obtained using <code>findIsotopes</code> .)
<code>rt.restrict</code>	Should lipid class retention time screening criteria be applied to putative compound assignments?
<code>rt.windows</code>	File path to a .csv file containing retention time "window" data to be used for screening by lipid class, if <code>rt.restrict = TRUE</code> . If nothing is specified, doLOBscreen will use the package default windows ( <code>default.rt.windows</code> ), which are specific to the HPLC-MS method currently used in the Van Mooy Lab at Woods Hole Oceanographic Institution.  Because the user is advised to provide retention time data specific to his/her HPLC-MS method, failure to specify a value for <code>rt.windows</code> will result in a warning. A Microsoft Excel spreadsheet template included with the package at <code>Resources/library/LOBSTAHS/doc/xlsx/LOBSTAHS_rt.windows.xlsx</code> can be used to generate a .csv file of retention time data in a format appropriate for <code>rt.windows</code> . Alternatively, the spreadsheet file may be downloaded <a href="#">from the package GitHub repository</a> .
<code>exclude.oddFA</code>	Should compound assignments with an odd total number of acyl carbon atoms be excluded? (Applies only to assignments where the parent lipid class is TAG, IP-DAG, PUA, FFA or IP-MAG.) Useful if data are (or are believed to be) exclusively eukaryotic origin.
<code>match.ppm</code>	$m/z$ tolerance (in ppm) used for matching observed data against the calculated $m/z$ 's in the database
<code>exclude.oxyrule</code>	Should compound assignments include physically unlikely fatty acid molecules in which the total number of double bonds is less than the oxidation state of the molecule? Useful if such rare molecules are likely to be found in sample. Exclusion applies only to assignments where the parent lipid class is TAG, IP-DAG, PUA, FFA or IP-MAG.
<code>retain.unidentified</code>	Should data for unidentified or discarded features be retained and appended to user's results? Useful if untargeted follow-on data analysis is anticipated, or when user wants to retain data for <i>all</i> features present in the original dataset, not just those for which a LOBSTAHS identity was found.

## Details

doLOBscreen draws compound identities from a LOBdbase database. The function applies various retention time and adduct ion hierarchy screening criteria to winnow the list of putative compound assignments. It returns a table of annotated peak data with compound assignments and various annotation codes to assist the user in interpretation and follow-on data analysis.

## Value

A "LOBSet-class" object.

## Author(s)

James Collins, <james.r.collins@aya.yale.edu>

## References

The LOBSTAHS package is presented in:

Collins, J.R., B.R. Edwards, H.F. Fredricks, and B.A.S. Van Mooy. 2016. LOBSTAHS: An adduct-based lipidomics strategy for discovery and identification of oxidative stress biomarkers. *Analytical Chemistry* 88:7154-7162, doi:[10.1021/acs.analchem.6b01260](https://doi.org/10.1021/acs.analchem.6b01260).

Data for lipid classes BLL, PDPT, vGSL, sGSL, hGSL, hapGSL, and hapCER are as described in:

Hunter J. E., M. J. Frada, H. F. Fredricks, A. Vardi, and B. A. S. Van Mooy. 2015. Targeted and untargeted lipidomics of *Emiliana huxleyi* viral infection and life cycle phases highlights molecular biomarkers of infection, susceptibility, and ploidy. *Frontiers in Marine Science* 2:81, doi:[10.3389/fmars.2015.00081](https://doi.org/10.3389/fmars.2015.00081)

Fulton, J. M., H. F. Fredricks, K. D. Bidle, A. Vardi, B. J. Kendrick, G. R. DiTullio, and B. A. S. Van Mooy. 2014. Novel molecular determinants of viral susceptibility and resistance in the lipidome of *Emiliana huxleyi*, *Environmental Microbiology* 16(4):1137-1149, doi:[10.1111/1462-2920.12358](https://doi.org/10.1111/1462-2920.12358).

## See Also

[LOBSet](#), [LOBdbase](#), [loadLOBdbase](#), [getLOBpeaklist](#), [generateLOBdbase](#), [default.LOBdbase](#), [default.rt.windows](#), [xcmsSet](#), [xsAnnotate](#), [findIsotopes](#)

## Examples

```
## screen & annotate xsAnnotate object from the Pth202lipids dataset using all
## screening options, while retaining unidentified/discarded features
library(Pth202lipids)

myPth202LOBSet = doLOBscreen(pth202lipids$xsAnnotate, polarity = "positive",
                             database = NULL, remove.iso = TRUE,
                             rt.restrict = TRUE, rt.windows = NULL,
                             exclude.oddFA = TRUE, match.ppm = 2.5,
                             exclude.oxyrule = TRUE, retain.unidentified = TRUE)

## show some diagnostics
LOBscreen_diagnostics(myPth202LOBSet) # screening diagnostics
```

```
LOBisoID_diagnostics(myPtH202LOBSet) # isomer identification data
```

---

exportDBtoCSV

*Export a LOBSTAHS database (LOBdbase) object to a text file*

---

## Description

Collects all elements of a [LOBdbase-class](#) object into a single table, then writes the table to a .csv file.

## Usage

```
exportDBtoCSV(LOBdbase)
```

## Arguments

LOBdbase      A LOBSTAHS "LOBdbase" object.

## Details

exportDBtoCSV extracts data from all slots in a given "LOBdbase" object and flows it into a data frame. The data frame is then written to a .csv file with a series of plain-language column headers. The file name includes the database polarity mode and a timestamp (in user's local time) indicating the time and date of export.

## Value

A .csv file containing data from a [LOBdbase-class](#) object.

## Author(s)

James Collins, <james.r.collins@aya.yale.edu>

## References

Collins, J.R., B.R. Edwards, H.F. Fredricks, and B.A.S. Van Mooy. 2016. LOBSTAHS: An adduct-based lipidomics strategy for discovery and identification of oxidative stress biomarkers. *Analytical Chemistry* 88:7154-7162

## See Also

[LOBdbase](#), [LOBdbase](#), [generateLOBdbase](#)

## Examples

```
## export default positive mode database to a text file

data("default.LOBdbase")

exportDBtoCSV(default.LOBdbase$positive)

## file is written to user's working directory, with filename containing
## polarity and timestamp of generation
```

---

extractLOBdbasedata    *Extract compound data from a LOBdbase*

---

## Description

Extracts data from a LOBSTAHS [LOBdbase-class](#) object for a given molecular species.

## Usage

```
extractLOBdbasedata(frag_ID, database)
```

## Arguments

frag_ID	The LOBdbase fragment ID(s) corresponding to the species for which data should be extracted.
database	The LOBdbase from which data are to be extracted.

## Value

A data frame containing the extracted data, with field names corresponding to the slots in database.

## Author(s)

James Collins, <james.r.collins@aya.yale.edu>

## References

Collins, J.R., B.R. Edwards, H.F. Fredricks, and B.A.S. Van Mooy. 2016. LOBSTAHS: An adduct-based lipidomics strategy for discovery and identification of oxidative stress biomarkers. *Analytical Chemistry* 88:7154-7162

## See Also

[LOBdbase](#), [LOBdbase loadLOBdbase](#), [generateLOBdbase](#), [default.LOBdbase](#)

## Examples

```
## extract data from the default database for the [M+H]+ adduct of
## dinitrophenyl-phosphatidylethanolamine (DNPPE), a synthetic lipid used as an
## internal standard

data(default.LOBdbase)

DNPPE.data = extractLOBdbasedata(frag_ID = 19801,
                                database = default.LOBdbase$positive)
```

---

generateLOBdbase

*Conduct in silico simulation and generate lipid-oxylipin database*

---

## Description

Applies an *in silico* simulation to generate data by ionization mode (polarity) for a wide range of lipids, oxidized lipids, and oxylipins. User-supplied structural criteria and empirically-determined adduct ion abundance rankings for the major lipid classes are used to create entries for a range of lipid moieties. The database(s) can then be used in [dolOBscreen](#) to assign compound identities to grouped peakdata.

## Usage

```
generateLOBdbase(polarity = c("positive", "negative"), gen.csv = FALSE,
                 component.defs = NULL, AIH.defs = NULL, acyl.ranges = NULL,
                 oxy.ranges = NULL)
```

## Arguments

polarity	Ionization mode for which database is to be generated.
gen.csv	Should results also be written to a .csv file?
component.defs	File path to a .csv file containing elemental composition definitions for the various chemical components needed by generateLOBdbase. If nothing is specified, generateLOBdbase will use the default composition table ( <a href="#">default.componentCompTable</a> ). The default table includes definitions for the masses of a wide range of adducts, photosynthetic pigments, and structural backbones of some major lipid classes. A Microsoft Excel spreadsheet template included with the package at <code>Resources/library/LOBSTAHS/doc/</code> can be used to generate a .custom csv file with elemental composition definitions in a format appropriate for generateLOBdbase. Alternatively, the spreadsheet may be downloaded <a href="#">from the package GitHub repository</a> . Brief instructions for customization of the table are given in this help document; full instructions, including details on specification of the necessary base fragment, are contained in <a href="#">the package vignette</a> . For each lipid class or compound specified in the component definitions table, the field <code>DB_gen_compound_type</code> must contain one of five values: "DB_acyl_iteration,"

"DB\_unique\_species," "basic\_component," "adduct\_pos," or "adduct\_neg." The last three compound types are reserved for definition of basic components such as acetonitrile or acetate and for definition of adduct ion types; new entries of these types should only be created in the compound table when a new adduct or basic component must be specified. The first two compound types are used to define the way generateLOBdbase creates its databases. There are essentially two ways generateLOBdbase creates database entries in LOBSTAHS.

For compounds of DB\_gen\_compound\_type = "DB\_unique\_species" (the simpler of the two cases), database entries will be created only for adduct ions of the single compound specified. The latter type should be used for pigments and other lipids that do not have acyl groups, or when the user does not wish to consider any possible variation in acyl properties. In this case, the exact mass of the complete (neutral) molecule should be specified in the component definitions (i.e., component composition) table.

Alternatively, for compounds of DB\_gen\_compound\_type = "DB\_acyl\_iteration", generateLOBdbase will create database entries for adduct ions of multiple molecular species within the lipid class based on the ranges of acyl properties and oxidation states given for the class in acyl\_ranges and oxy\_ranges (see below). In this case, the compound table should be used to define the exact mass of a "base fragment" for the lipid class. Using this "base fragment" as a starting point, generateLOBdbase creates multiple entries for molecules in the lipid class by iterative addition of various combinations of fatty acids. In the case of IP-DAG and IP-MAG, the base fragment includes the entire polar headgroup, the glycerol backbone, and both carboxylic oxygen atoms in the fatty acid(s). In the case of TAG, the base fragment is defined as the glycerol backbone plus the carboxylic oxygen atoms on each of the three fatty acids. The base fragments for any new lipid classes for which the user desires evaluation of a range of acyl properties should be similarly defined.

Note that regardless of the DB\_gen\_compound\_type, an adduct hierarchy **must** be specified in the adduct ion hierarchy matrix (see below) for each compound or compound class specified in the Adduct\_hierarchy\_lookup\_class field of the component definitions table.

**AIH.defs** File path to a .csv file containing empirical adduct ion hierarchy (AIH) data for various pigments, lipids, and lipid classes. If nothing is specified, generateLOBdbase will use the default AIH data ([default.adductHierarchies](#)). Each compound or compound class for which there is an entry in the AIH definitions table should have at least one corresponding entry in the Adduct\_hierarchy\_lookup\_class field of the component definitions table (default, [default.componentCompTable](#)).

A Microsoft Excel spreadsheet template included with the package at Resources/library/LOBSTAHS/doc/ can be used to generate a .csv file with additional (or alternative) adduct hierarchy data in a format appropriate for generateLOBdbase. Alternatively, the spreadsheet may be downloaded [from the package GitHub repository](#).

**acyl\_ranges** File path to a .csv file containing ranges of values for the total number of acyl (i.e., fatty acid) carbon atoms to be considered during the *in silico* simulation of any lipid classes for which DB\_gen\_compound\_type is specified as "DB\_acyl\_iteration" in the component definitions table, above. These include intact polar diacylglycerols (IP-DAG), triacylglycerols (TAG), polyunsaturated

aldehydes (PUAs), and free fatty acids (FFA). If nothing is specified, generateLOBdbase will use the default acyl carbon atom range data in ([default.acylRanges](#)).

A Microsoft Excel spreadsheet template included with the package at Resources/library/LOBSTAHS/doc/ can be used to generate a .csv file with custom acyl carbon range data in a format appropriate for generateLOBdbase. Alternatively, the spreadsheet may be downloaded [from the package GitHub repository](#).

oxy.ranges

File path to a .csv file containing ranges of values for the number of additional oxygen atoms to be considered during the *in silico* simulation of any lipid classes for which DB\_gen\_compound\_type is specified as "DB\_acyl\_iteration" in the component definitions table, above. If nothing is specified, generateLOBdbase will use the default oxidation state ranges in ([default.oxyRanges](#)).

A Microsoft Excel spreadsheet template included with the package at Resources/library/LOBSTAHS/doc/ can be used to generate a .csv file with custom oxidation state ranges in a format appropriate for generateLOBdbase. Alternatively, the spreadsheet may be downloaded [from the package GitHub repository](#). By default, generateLOBdbase considers 0-4 additional oxygen atoms on each chemically possible IP-DAG, TAG, PUA, and FFA.

## Details

Using the default structural property inputs described here, generateLOBdbase can produce databases with entries for a wide range of intact polar diacylglycerols (IP-DAG), triacylglycerols (TAG), polyunsaturated aldehydes (PUAs), free fatty acids (FFA), and common photosynthetic pigments. The default databases (as of January 2017) contain data on 18,067 and 15,404 unique compounds that can be identified in positive and negative ion mode spectra, respectively.

**Note** that the default databases have been pre-generated (see [default.LOBdbase](#)) and it is therefore unnecessary to call generateLOBdbase with the default parameters.

## Value

A "[LOBdbase-class](#)" object with the structure:

frag\_ID: Object of class "integer", a unique identifier for this molecular species

mz: Object of class "numeric", the calculated  $m/z$  of this species

exact\_parent\_neutral\_mass: Object of class "numeric", the calculated (monoisotopic) exact mass of the parent compound of this species

lipid\_class: Object of class "factor", the parent lipid class of this species

species: Object of class "character", the lipid subclass

adduct: Object of class "factor", the adduct ion represented by this entry

adduct\_rank: Object of class "integer", the relative abundance ranking of this adduct relative to the other adducts of the same parent compound

FA\_total\_no\_C: Object of class "integer", total number of acyl (fatty acid) carbon atoms in the parent compound; NA if lipid\_class is not TAG, IP-DAG, PUA, or FFA

FA\_total\_no\_DB: Object of class "integer", total number of acyl (fatty acid) carbon-carbon double bonds in the parent compound; NA if lipid\_class is not TAG, IP-DAG, PUA, or FFA

degree\_oxidation: Object of class "integer", number of additional oxygen atoms present



---

getLOBpeaklist	<i>Export screened LOBSTAHS peaklist with compound assignments</i>
----------------	--------------------------------------------------------------------

---

### Description

Extracts screened peak data, compound assignments, annotation codes, and (optionally) isomer data from a `LOBSet-class` object. Returns a table containing the requested data, with option to export to a .csv file.

### Usage

```
getLOBpeaklist(LOBSet, include.iso = TRUE, include.unidentified = TRUE,  
               gen.csv = FALSE)
```

### Arguments

<code>LOBSet</code>	A LOBSTAHS "LOBSet" object.
<code>include.iso</code>	Specify whether isomer and isobar identification data should be included in peaklist.
<code>include.unidentified</code>	If data for unidentified or discarded features is present in the LOBSet, should these data be exported with the peaklist? A value of FALSE will yield a peaklist that includes data only for those features to which one or more LOBSTAHS compound identities have been assigned.
<code>gen.csv</code>	Should a .csv file be generated in addition to the data frame that is returned?

### Details

`getLOBpeaklist` extracts data from all slots in a given "LOBSet" object and flows it into a data frame. Annotation codes indicating compliance with the adduct ion hierarchy screening criteria are appended to the *m/z*, retention time, and peak area data for each xcms peakgroup remaining in the final dataset.

If `include.iso = TRUE`, three additional columns containing the `match_IDs` of the possible isomers and isobars for each peakgroup are also appended. `getLOBpeaklist` does not export any of the diagnostic data in the LOBSet `LOBscreen_diagnostics` or `LOBisoID_diagnostics` slots.

When the LOBSet includes peak data for features that were not identified during screening or were discarded (i.e., if the user specified `retain.unidentified = TRUE` when calling `doLOBscreen`), the user is given the option to export these data when using `getLOBpeaklist`. This is useful when untargeted follow-on data analysis is anticipated, or the user simply wants to export data for *all* features present in the original dataset, not just those for which a LOBSTAHS identity was found.

### Value

A data frame with the following structure:

match\_ID: Object of class "integer", unique identifier for each assignment of a compound to a peakgroup (multiple match\_IDs can exist for a peakgroup if the group was assigned multiple compound identities)

compound\_name: Object of class "character", name of compound; see reference for naming convention applied to compounds other than pigments

elem\_formula: Object of class "character", empirical formula of compound

LOBdbase\_mz: Object of class "numeric", calculated  $m/z$  of the adduct for which data in this group are reported; obtained database

peakgroup\_mz: Object of class "numeric", mean observed  $m/z$  of the feature in this peakgroup across all samples in which it was identified

LOBdbase\_ppm\_match: Object of class "numeric", ppm deviation between observed and calculated  $m/z$

peakgroup\_rt: Object of class "numeric", mean observed retention time of the feature in this peakgroup across all samples in which it was identified

peakgroup\_mzmin: Object of class "numeric", minimum observed  $m/z$  of feature across samples

peakgroup\_mzmax: Object of class "numeric", maximum observed  $m/z$  of feature across samples

peakgroup\_rtmin: Object of class "numeric", minimum observed retention time of feature across samples

peakgroup\_rtmax: Object of class "numeric", maximum observed retention time of feature across samples

**peak area data:** Several objects of class "numeric", containing integrated peak area data for this group by sample (one column for each sample in the dataset)

xcms\_peakgroup: Object of class "integer", the xcms xcmsSet peakgroup identifier

CAMERA\_pseudospectrum: Object of class "integer", the CAMERA xsAnnotate pseudospectrum identifier

LOBdbase\_frag\_ID: Object of class "integer", the LOBdbase fragment ID corresponding to the adduct of this compound for which data are reported; this is the dominant adduct of the compound according to the adduct ion hierarchy rules for the parent lipid class

LOBdbase\_exact\_parent\_neutral\_mass: Object of class "numeric", the calculated exact (monoisotopic) mass of the compound; from database

lipid\_class: Object of class "factor", parent lipid class of this compound

species: Object of class "character", if a pigment or IP-DAG, the specific compound species

major\_adduct: Object of class "factor", adduct of the compound for which data in this entry is reported

FA\_total\_no\_C: Object of class "integer", total number of acyl (fatty acid) carbon atoms in this compound; "NA" if lipid\_class is not TAG, IP-DAG, PUA, or FFA

FA\_total\_no\_DB: Object of class "integer", total number of acyl (fatty acid) carbon-carbon double bonds in this compound; "NA" if lipid\_class is not TAG, IP-DAG, PUA, or FFA

degree\_oxidation: Object of class "integer", number of additional oxygen atoms present on this compound, compared with its unoxidized parent

C1-C6b: Several objects of class "integer", containing binary indicators for each possible annotation code applied by doLOBscreen

**casecodes:** Object of class "character", character string containing list of all codes applied to this assignment

**iso\_C3r\_match\_ID:** Object of class "character", character string of integer containing the match\_IDs of all possible regioisomers of this compound (if `include.iso = TRUE`)

**iso\_C3f\_match\_ID:** Object of class "character", character string of integer containing the match\_IDs of all possible functional structural isomers of this compound (if `include.iso = TRUE`)

**iso\_C3c\_match\_ID:** Object of class "character", character string of integer containing the match\_IDs of all possible isobars of this compound (if `include.iso = TRUE`)

### Author(s)

James Collins, <james.r.collins@aya.yale.edu>

### References

Collins, J.R., B.R. Edwards, H.F. Fredricks, and B.A.S. Van Mooy. 2016. LOBSTAHS: An adduct-based lipidomics strategy for discovery and identification of oxidative stress biomarkers. *Analytical Chemistry* 88:7154-7162

### See Also

[LOBSet](#), [LOBSet](#), [doLOBscreen](#)

### Examples

```
## export peaklist, with isomer data, but without data for unidentified features
library(PtH202lipids)
```

```
PtH202.peakdata = getLOBpeaklist(pth202lipids$LOBSet, include.iso = TRUE,
                                include.unidentified = FALSE, gen.csv = FALSE)
```

---

loadLOBdbase

*Import and reconstruct LOBdbase from a text file*

---

### Description

Reconstruct a "LOBdbase" object from properly formatted data in a .csv file. More robust than the generic constructor function [LOBdbase](#).

### Usage

```
loadLOBdbase(file, polarity, num_compounds = NULL)
```

## Arguments

file	Path to a .csv file containing the database to be imported. The file format should be consistent with the .csv output that is obtained using <code>gen.csv = TRUE</code> in <a href="#">generateLOBdbase</a> . Some leeway is allowed for variation in capitalization and punctuation of column headers.
polarity	Specify polarity (ionization mode) of the database being imported ("positive" or "negative"). <code>loadLOBdbase</code> will attempt to detect the polarity mode based on data in the "adduct" column if nothing is given.
num_compounds	If known, the number of parent compounds represented in the database being imported. Can be unspecified.

## Details

`loadLOBdbase` is a glorified implementation of [read.table](#) that attempts to determine whether the format of the data in `file` is consistent with that of a saved "LOBdbase" object. Some leeway is allowed for variation in punctuation and spelling of column headers in the source file. Special attention should be paid to how adduct ions are specified (e.g., "[M+H]+", "[M+NH4]+", or "[M+C1]-"). Most users will find this function more useful than the generic constructor function [LOBdbase](#).

## Value

A "[LOBdbase-class](#)" object.

## Author(s)

James Collins, <james.r.collins@aya.yale.edu>

## References

Collins, J.R., B.R. Edwards, H.F. Fredricks, and B.A.S. Van Mooy. 2016. LOBSTAHS: An adduct-based lipidomics strategy for discovery and identification of oxidative stress biomarkers. *Analytical Chemistry* 88:7154-7162

## See Also

[LOBdbase](#), [LOBdbase](#), [doLOBscreen](#), [generateLOBdbase](#), [default.LOBdbase](#)

## Examples

```
## save the default negative mode database as a .csv file

data(default.LOBdbase)

neg.DB = default.LOBdbase$negative

fname = paste0("LOBSTAHS_lipid-oxy_DB_",
               strtrim(as.character(polarity(neg.DB)),3), ".csv")

exportmat = data.frame(frag_ID(neg.DB),
                       mz(neg.DB),
```

```

exact_parent_neutral_mass(neg.DB),
as.character(lipid_class(neg.DB)),
as.character(species(neg.DB)),
as.character(adduct(neg.DB)),
as.character(adduct_rank(neg.DB)),
FA_total_no_C(neg.DB),
FA_total_no_DB(neg.DB),
degree_oxidation(neg.DB),
parent_elem_formula(neg.DB),
parent_compound_name(neg.DB),
stringsAsFactors = FALSE)

colnames(exportmat) = c("frag_ID", "mz", "exact_parent_neutral_mass",
"lipid_class", "species", "adduct", "adduct_rank",
"FA_total_no_C", "FA_total_no_DB", "degree_oxidation",
"parent_elem_formula", "parent_compound_name")

write.csv(exportmat, fname)

## reimport it

neg.DB.reimported = loadLOBdbase("LOBSTAHS_lipid-oxy_DB_neg.csv",
polarity = "negative",
num_compounds = NULL)

```

---

LOBdbase

*LOBdbase constructor for manual creation or reconstruction of a  
LOBdbase object*


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## Description

Constructor function for manual assembly or reconstruction of a LOBdbase object to be used in screening data with the LOBSTAHS function [doLOBscreen](#).

## Usage

```

LOBdbase(frag_ID = NULL, mz = NULL, exact_parent_neutral_mass = NULL,
lipid_class = NULL, species = NULL, adduct = NULL, adduct_rank = NULL,
FA_total_no_C = NULL, FA_total_no_DB = NULL, degree_oxidation = NULL,
parent_elem_formula = NULL, parent_compound_name = NULL,
polarity = NULL, num_entries = NULL, num_compounds = NULL)

```

## Arguments

frag_ID	An object of class "integer"; vector of unique identifiers for the molecular species in the database.
mz	An object of class "numeric"; calculated $m/z$ of each species for which an entry exists.

<code>exact_parent_neutral_mass</code>	An object of class "numeric"; calculated (monoisotopic) exact masses of the parent compound of each species.
<code>lipid_class</code>	An object of class "factor"; parent lipid classes of each species
<code>species</code>	An object of class "character"; the lipid subclasses of each species
<code>adduct</code>	An object of class "factor"; the adduct ions represented by each entry
<code>adduct_rank</code>	An object of class "integer"; the relative abundance rankings of each adduct relative to the other adducts of the same parent compound
<code>FA_total_no_C</code>	An object of class "integer"; the total number of acyl (fatty acid) carbon atoms in the parent compound of each entry; values should be NA where <code>lipid_class</code> is not TAG, IP-DAG, PUA, or FFA
<code>FA_total_no_DB</code>	An object of class "integer"; the total number of acyl (fatty acid) carbon-carbon double bonds in the parent compound of each entry; values should be NA where <code>lipid_class</code> is not TAG, IP-DAG, PUA, or FFA
<code>degree_oxidation</code>	An object of class "integer"; the number of additional oxygen atoms present on each species
<code>parent_elem_formula</code>	An object of class "character"; the elemental formulae of the parent compound of each species
<code>parent_compound_name</code>	An object of class "character"; names of the parent compound of each species; see the reference for this entry for naming conventions that should be applied for pigments and compounds other than pigments
<code>polarity</code>	An object of class "factor" with length = 1; the ionization mode of data in the database to be constructed
<code>num_entries</code>	An object of class "integer" with length = 1; the number of total entries (adducts) in the database to be constructed. If specified, the value of <code>num_entries</code> should be equal to the length of any arguments that contain database data
<code>num_compounds</code>	An object of class "integer" with length = 1; the number of parent compounds represented in the database to be constructed. If specified, the value of <code>num_compounds</code> should be < the value specified for <code>num_entries</code> .

## Details

Typically, a LOBdbase will be created using the in silico simulation function [generateLOBdbase](#). Formatted database entries (such as from an external .csv file) can be loaded using [loadLOBdbase](#). The rudimentary LOBdbase constructor function is therefore provided only for manual object creation; it will not be needed by most users. All arguments except for those containing metadata (i.e., `polarity`, `num_entries`, and `num_compounds`) should be of the same length.

## Value

A "LOBdbase-class" object.

**Author(s)**

James Collins, <james.r.collins@aya.yale.edu>

**References**

The LOBSTAHS package is presented in:

Collins, J.R., B.R. Edwards, H.F. Fredricks, and B.A.S. Van Mooy. 2016. LOBSTAHS: An adduct-based lipidomics strategy for discovery and identification of oxidative stress biomarkers. *Analytical Chemistry* 88:7154-7162, doi:[10.1021/acs.analchem.6b01260](https://doi.org/10.1021/acs.analchem.6b01260).

Data for lipid classes BLL, PDPT, vGSL, sGSL, hGSL, hapGSL, and hapCER are as described in: Hunter J. E., M. J. Frada, H. F. Fredricks, A. Vardi, and B. A. S. Van Mooy. 2015. Targeted and untargeted lipidomics of *Emiliana huxleyi* viral infection and life cycle phases highlights molecular biomarkers of infection, susceptibility, and ploidy. *Frontiers in Marine Science* 2:81, doi:[10.3389/fmars.2015.00081](https://doi.org/10.3389/fmars.2015.00081)

Fulton, J. M., H. F. Fredricks, K. D. Bidle, A. Vardi, B. J. Kendrick, G. R. DiTullio, and B. A. S. Van Mooy. 2014. Novel molecular determinants of viral susceptibility and resistance in the lipidome of *Emiliana huxleyi*, *Environmental Microbiology* 16(4):1137-1149, doi:[10.1111/1462-2920.12358](https://doi.org/10.1111/1462-2920.12358).

**See Also**

[generateLOBdbase](#), [loadLOBdbase](#), [doLOBscreen](#), [LOBdbase](#)

**Examples**

```
## create an empty LOBdbase

myLOBdbase = LOBdbase(frag_ID = NULL, mz = NULL,
                      exact_parent_neutral_mass = NULL, lipid_class = NULL,
                      species = NULL, adduct = NULL, adduct_rank = NULL,
                      FA_total_no_C = NULL, FA_total_no_DB = NULL,
                      degree_oxidation = NULL, parent_elem_formula = NULL,
                      parent_compound_name = NULL, polarity = NULL,
                      num_entries = NULL, num_compounds = NULL)
```

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LOBdbase-class

*Class LOBdbase: A class for LOBSTAHS lipid-oxylipin databases*

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**Description**

A class for LOBSTAHS databases that contain a combination of *in silico* and empirical data for a wide range of lipids, oxidized lipids, and oxylipins.

**Objects from the class**

Objects can be created using the simulation function [generateLOBdbase](#) (preferred; satisfies the needs of most users), imported from a .csv file of proper format using [loadLOBdbase](#), or created using the rudimentary constructor [LOBdbase](#) (least preferred). A 'LOBdbase' can also be created by calls of the form `new("LOBdbase", ...)`.

**Slots**

**frag\_ID**: Object of class "integer", a unique identifier for this molecular species  
**mz**: Object of class "numeric", the calculated  $m/z$  of this species  
**exact\_parent\_neutral\_mass**: Object of class "numeric", the calculated (monoisotopic) exact mass of the parent compound of this species  
**lipid\_class**: Object of class "factor", the parent lipid class of this species  
**species**: Object of class "character", the lipid subclass  
**adduct**: Object of class "factor", the adduct ion represented by this entry  
**adduct\_rank**: Object of class "integer", the relative abundance ranking of this adduct relative to the other adducts of the same parent compound  
**FA\_total\_no\_C**: Object of class "integer", total number of acyl (fatty acid) carbon atoms in the parent compound; NA if lipid\_class is not TAG, IP-DAG, PUA, or FFA  
**FA\_total\_no\_DB**: Object of class "integer", total number of acyl (fatty acid) carbon-carbon double bonds in the parent compound; NA if lipid\_class is not TAG, IP-DAG, PUA, or FFA  
**degree\_oxidation**: Object of class "integer", number of additional oxygen atoms present  
**parent\_elem\_formula**: Object of class "character", elemental formula of the parent compound  
**parent\_compound\_name**: Object of class "character", name of the parent compound; see the reference for this entry for the naming convention applied to compounds other than pigments  
**polarity**: Object of class "factor", ionization mode of data in the database  
**num\_entries**: Object of class "integer", number of total entries (adducts) in the database  
**num\_compounds**: Object of class "integer", number of parent compounds represented in the database (should be < num\_entries)

**Methods**

**show** signature(object = "LOBdbase"): ...  
**polarity** signature(object = "LOBdbase"): get polarity slot  
**num\_compounds** signature(object = "LOBdbase"): get num\_compounds slot  
**num\_entries** signature(object = "LOBdbase"): get num\_entries slot  
**frag\_ID** signature(object = "LOBdbase"): get frag\_ID slot  
**exact\_parent\_neutral\_mass** signature(object = "LOBdbase"): get exact\_parent\_neutral\_mass slot  
**lipid\_class** signature(object = "LOBdbase"): get lipid\_class slot  
**species** signature(object = "LOBdbase"): get species slot  
**adduct** signature(object = "LOBdbase"): get adduct slot  
**adduct\_rank** signature(object = "LOBdbase"): get adduct\_rank slot  
**FA\_total\_no\_C** signature(object = "LOBdbase"): get FA\_total\_no\_C slot  
**FA\_total\_no\_DB** signature(object = "LOBdbase"): get FA\_total\_no\_DB slot  
**degree\_oxidation** signature(object = "LOBdbase"): get degree\_oxidation slot  
**parent\_elem\_formula** signature(object = "LOBdbase"): get parent\_elem\_formula slot  
**parent\_compound\_name** signature(object = "LOBdbase"): get parent\_compound\_name slot

**Author(s)**

James Collins, <james.r.collins@aya.yale.edu>

**References**

Collins, J.R., B.R. Edwards, H.F. Fredricks, and B.A.S. Van Mooy. 2016. LOBSTAHS: An adduct-based lipidomics strategy for discovery and identification of oxidative stress biomarkers. *Analytical Chemistry* 88:7154-7162

**See Also**

[generateLOBdbase](#), [loadLOBdbase](#), [doLOBscreen](#), [LOBdbase](#)

**Examples**

```
## return object information  
  
showClass("LOBdbase")
```

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LOBdefaults

*LOBSTAHS default databases and database generation parameters*

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**Description**

Default databases (in `default.LOBdbase`), and the `.RData` files containing default ranges of structural properties used by [generateLOBdbase](#) to generate these databases.

Note that the format of these files has changed in LOBSTAHS version 1.1.2 and greater.

Also described is `default.rt.windows`, which contains the default retention time windows (by lipid class) used by [doLOBscreen](#) when `rt.restrict = TRUE`.

**Usage**

```
data(default.LOBdbase)  
data(default.adductHierarchies)  
data(default.acylRanges)  
data(default.oxyRanges)  
data(default.componentCompTable)  
data(default.rt.windows)
```

**Format**

`default.LOBdbase` A list of two "LOBdbase" objects, which are the default LOBSTAHS databases for positive and negative ion mode species, respectively. These were generated using [generateLOBdbase](#) with the default values defined in `default.adductHierarchies`, `default.acylRanges`, `default.oxyRanges`, and `default.componentCompTable`.

`default.adductHierarchies` A data frame containing empirically-determined adduct ion hierarchy data, by lipid class.

`default.acylRanges` A data frame containing ranges of numbers of acyl carbon atoms for which *in silico* data are generated for each lipid class by [generateLOBdbase](#).

`default.oxyRanges` A data frame containing ranges of additional oxygen atoms to be considered on species of each lipid class when databases are generated with [generateLOBdbase](#).

`default.componentCompTable` A data frame that defines the elemental compositions of the various adducts, parent lipid "backbones," and pigments that are used by [generateLOBdbase](#).

`default.rt.windows` A data frame containing the default retention time data for various lipids and parent lipid classes that are used by [doLOBscreen](#) when `rt.restrict = TRUE`. These retention time windows are specific to the HPLC-MS method currently used in the Van Mooy Lab at Woods Hole Oceanographic Institution, where LOBSTAHS was developed. As described in [doLOBscreen](#), users outside the Van Mooy Lab should supply their own retention time data.

## Details

Empirical determination of the retention time window data in `default.rt.windows` and adduct ion hierarchies in `default.adductHierarchies` are described in the references below.

The default ranges for the structural properties given in the other files were chosen to yield databases that encompass a broad variety of moieties across lipid types. Microsoft Excel spreadsheet templates are included with the package in `Resources/library/LOBSTAHS/doc` for users wishing to modify any of the default data inputs. Alternatively, the spreadsheet files may be downloaded [from a directory embedded within the package](#). These templates can be used to generate .csv files in formats appropriate for [generateLOBdbase](#) and [doLOBscreen](#).

## Value

Various list and data.frame objects (as indicated above).

## Source

<http://github.com/vanmooylipidomics/LOBSTAHS/>

## References

The LOBSTAHS package is presented in:

Collins, J.R., B.R. Edwards, H.F. Fredricks, and B.A.S. Van Mooy. 2016. LOBSTAHS: An adduct-based lipidomics strategy for discovery and identification of oxidative stress biomarkers. *Analytical Chemistry* 88:7154-7162, doi:[10.1021/acs.analchem.6b01260](https://doi.org/10.1021/acs.analchem.6b01260).

Data for lipid classes BLL, PDPT, vGSL, sGSL, hGSL, hapGSL, and hapCER are as described in:

Hunter J. E., M. J. Frada, H. F. Fredricks, A. Vardi, and B. A. S. Van Mooy. 2015. Targeted and untargeted lipidomics of *Emiliana huxleyi* viral infection and life cycle phases highlights molecular biomarkers of infection, susceptibility, and ploidy. *Frontiers in Marine Science* 2:81, doi:[10.3389/fmars.2015.00081](https://doi.org/10.3389/fmars.2015.00081)

Fulton, J. M., H. F. Fredricks, K. D. Bidle, A. Vardi, B. J. Kendrick, G. R. DiTullio, and B. A. S. Van Mooy. 2014. Novel molecular determinants of viral susceptibility and resistance in the lipidome of *Emiliana huxleyi*, *Environmental Microbiology* 16(4):1137-1149, doi:[10.1111/1462-2920.12358](https://doi.org/10.1111/1462-2920.12358).

**See Also**

[doLOBscreen](#), [generateLOBdbase](#), [LOBdbase](#) [LOBdbase](#)

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LOBSet	<i>LOBSet constructor for manual creation or reconstruction of a LOB-Set object</i>
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**Description**

Constructor function for manual creation or reconstruction of a LOBSet object for HPLC-MS peak data that have been screened using LOBSTAHS.

**Usage**

```
LOBSet(peakdata = NULL, iso_C3r = NULL, iso_C3f = NULL, iso_C3c = NULL,
       LOBscreen_diagnostics = NULL, LOBisoID_diagnostics = NULL,
       LOBscreen_settings = NULL, polarity = c("positive", "negative"),
       samppnames = NULL)
```

**Arguments**

peakdata	An object of class "data.frame" containing peak data and LOBSTAHS annotation information by assignment. Column headings and data types should conform to those of the peakdata slot of a <a href="#">LOBSet-class</a> object produced using the function <a href="#">doLOBscreen</a> . Each row in the peakdata table represents one compound assignment made by LOBSTAHS. The format of the data frame occupying the peakdata slot in a LOBSet object can be obtained using the <a href="#">peakdata</a> accessor for objects of <a href="#">LOBSet-class</a> .
iso_C3r	An object of class "list", a list of the match_IDs of possible regioisomers of each compound for which there is a row in peakdata. Length of iso_C3r should equal the number of rows in the data frame given for peakdata.
iso_C3f	An object of class "list", a list of the match_IDs of possible functional structural isomers of each compound for which there is a row in peakdata. Length of iso_C3f should equal the number of rows in the data frame given for peakdata.
iso_C3c	An object of class "list", a list of the match_IDs of the isobars of each compound for which there is a row in peakdata. Length of iso_C3c should equal the number of rows in the data frame given for peakdata.
LOBscreen_diagnostics	An object of class "data.frame", containing diagnostic information recorded by the function <a href="#">doLOBscreen</a> during creation of a <a href="#">LOBSet</a> . The numbers of peaks, peakgroups, adducts, and unique parent compounds present the dataset after application of each LOBSTAHS screening criterion.
LOBisoID_diagnostics	An object of class "data.frame", containing isomer and isobar summary statistics. The numbers of peakgroups and parent compounds to which the various isomer identifications have been applied by <a href="#">doLOBscreen</a> to a given LOBSet.

LOBscreen_settings	An object of class "list"; the settings used in <a href="#">doLOBscreen</a> to generate the LOBSet
polarity	An object of class "factor", polarity of data in the LOBSet. Must be either "negative" or "positive."
sampnames	An object of class "character"; the names of the samples from which the LOBSet was generated.

### Details

Typically, a LOBSet will be created from a CAMERA [xsAnnotate-class](#) object using the LOBSTAHS function [doLOBscreen](#). The LOBSet constructor function is therefore provided only for manual object creation; it will not be needed by most users.

### Value

A "LOBSet-class" object.

### Author(s)

James Collins, <james.r.collins@aya.yale.edu>

### References

Collins, J.R., B.R. Edwards, H.F. Fredricks, and B.A.S. Van Mooy. 2016. LOBSTAHS: An adduct-based lipidomics strategy for discovery and identification of oxidative stress biomarkers. *Analytical Chemistry* 88:7154-7162

### See Also

[LOBSet](#), [doLOBscreen](#), [xsAnnotate](#)

### Examples

```
## create an empty LOBSet for positive ion mode data

myLOBSet = LOBSet(peakdata = NULL, iso_C3r = NULL, iso_C3f = NULL,
                  iso_C3c = NULL, LOBscreen_diagnostics = NULL,
                  LOBisoID_diagnostics = NULL, LOBscreen_settings = NULL,
                  polarity = "positive", sampnames = NULL)
```

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LOBSet-class	<i>Class LOBSet: Peak data with annotations, isomers, and compound assignments</i>
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## Description

A class for HPLC-MS peak data that have been screened and annotated using LOBSTAHS function [doLOBscreen](#).

## Objects from the class

Objects can be created with the [LOBSet](#) constructor. A 'LOBSet' can also be created by calls of the form `new("LOBSet", ...)`.

## Slots

**peakdata:** Object of class "data.frame", containing peakdata by compound assignment

**iso\_C3r:** Object of class "list", a list of the match\_IDs of possible regioisomers of each compound

**iso\_C3f:** Object of class "list", a list of the match\_IDs of possible functional structural isomers of each compound

**iso\_C3c:** Object of class "list", a list of the match\_IDs of possible isobars of this compound

**LOBscreen\_diagnostics:** Object of class "data.frame", numbers of peaks, peakgroups, adducts, and unique parent compounds present in the dataset after application of each screening criterion in [doLOBscreen](#)

**LOBisoID\_diagnostics:** Object of class "data.frame", numbers of peakgroups and parent compounds to which the various isomer annotations have been assigned

**LOBscreen\_settings:** Object of class "list", captures the settings used in [doLOBscreen](#) to generate the "LOBSet"

**polarity:** Object of class "factor", polarity of data in the "LOBSet"

**samprnames:** Object of class "character", the names of the samples from which the "LOBSet" was generated

## Methods

**show** signature(object = "LOBSet"): ...

**LOBisoID\_diagnostics** signature(object = "LOBSet"): get LOBisoID\_diagnostics slot

**LOBscreen\_diagnostics** signature(object = "LOBSet"): get LOBscreen\_diagnostics slot

**LOBscreen\_settings** signature(object = "LOBSet"): get LOBscreen\_settings slot

**samprnames** signature(object = "LOBSet"): get samprnames slot

**peakdata** signature(object = "LOBSet"): get peakdata slot

**polarity** signature(object = "LOBSet"): get polarity slot

**Author(s)**

James Collins, <james.r.collins@aya.yale.edu>

**References**

Collins, J.R., B.R. Edwards, H.F. Fredricks, and B.A.S. Van Mooy. 2016. LOBSTAHS: An adduct-based lipidomics strategy for discovery and identification of oxidative stress biomarkers. *Analytical Chemistry* 88:7154-7162

**See Also**

[doLOBscreen](#), [getLOBpeaklist](#), [LOBSet](#), [xsAnnotate](#)

**Examples**

```
## return object information  
  
showClass("LOBSet")
```

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